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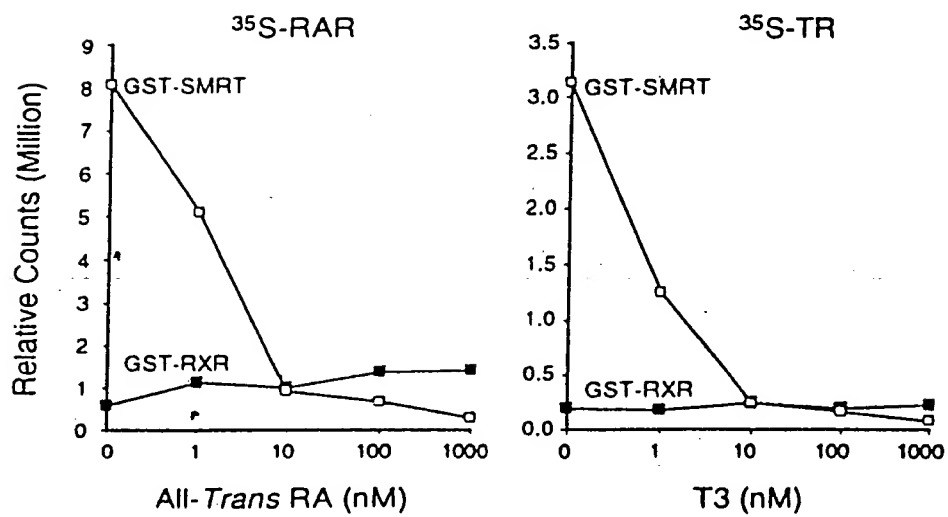


FIGURE 1



1 MEAWDAH@KEAFAAEAQKLEGGDEBCWTSGL@FEV@PREVIKAS@HAP@
51 SAFSYA@B@GH@L@LGLHDTAR@V@L@P@ET@ISN@E@L@ISSAKH@SVLERQI
101 GAISQGMSVQLHV@YSEHAKA@V@G@V@TMGL@L@L@MD@KKLA@FSGVKQEQ
151 SPRGQAGPPESLGVPTAQEASVLRGTALGSPVPGGSITKGIPSTRVPSDSA
201 ITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEG
251 KKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAI
301 SSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYLR
351 REAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAG
401 RSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHD
451 VRSLIGSPGRTPFPVHPLDVMADARALERACYEESLKSRPGTASSSGGSI
501 ARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEG
551 SLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPHISPYEHLRGVSGVD
601 LYRSHIPLAFDPTSI PRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRG
651 YPDAALENRQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLAL
701 NYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRH
751 SSSPLSPGGPHTLTKPTTTSSSERERDRDRERDREREKSILTSTTTVE
801 HAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTDALQ
851 QRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLG
901 GTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPA
951 SSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPH
1001 REKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK
1051 HLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPES@PSSSPLI@
1101 APGVKGH@RVVTLA@HISEVIT@DYTRHHE@LSAPLPAPLYSFPGASCP
1151 VLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGI
1201 EPVSPPEGMTPEGHSRSVAVYLLYRDGEQTEPSRMGSKSPGNTSQPPAFF

1251 SK@TESNSA@KSKKQ@INKKLNT@NRNEPEYNISQPGTEIFNMPAITGT

1301 GL@TYRSQA@EHASTNMGLEAIIRKALM@KYDQW.EESPPLSANAFNPL

1350 NASASLPAAMPITAADGRSDHTLTSP@.GGGGKAKVSGRPSSRKAKSPAPG

1399 LA..SGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPL@

1447 MRLQAG@MASPPPPG@PAGSG@..AGPHHA...WDEEPKPL@CSQYET@

FIGURE 2



FIGURE 3A

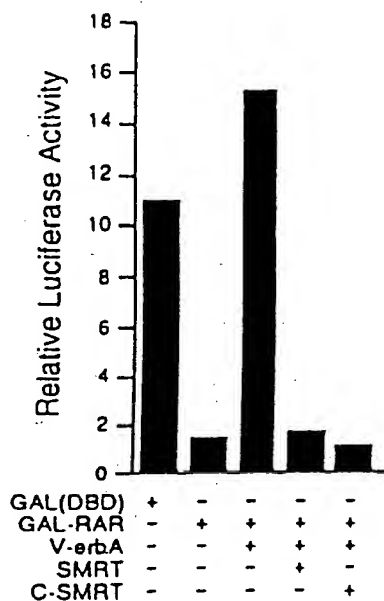


FIGURE 3B

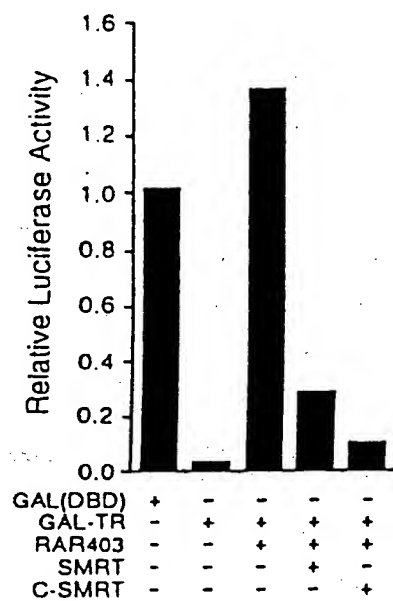


FIGURE 3C

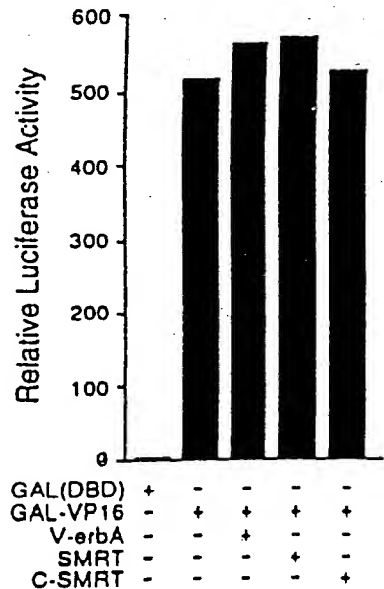
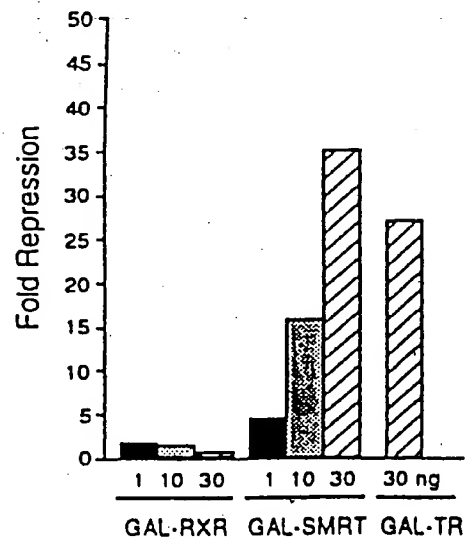


FIGURE 3D





MSGSTQLVAQTWRATEPRYPHSLSYVQIARTHTDVGLLLEYQHHSRDYASHLSPGSI IQPQRRRPSLLSEFPQGNERSQELHLRPESHSYLPELGKSEM
MSGSTQPVAQTWRAAEPRYPHSGISYVQIARSHTDVGLLLEYQHHPDYTHSLSPGSI IQPQRRRPSLLSEFPQGSERSQELHLRPSRTFLPELGKFDI

101 EFIESKRPRLELLPDPLLRPSLLATGQPSGSEDLT KDRLTGKLEPVSPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKKKKQQQL
101 EFTESKRPRLELLPDPLLRPSLLATGQPSGSEDLT KDRLTGKLEPVSPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKKKKQQQL

201 EEEAAKPPPEKPVSPPPIESKHRSVLQIIYDENRKAEEAHRILEGLGPQVELFLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKPCQ
201 EEEAAKPPPEKPVSPPPIESKHRSVLQIIYDENRKAEEAHRILEGLGPQVELFLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQRFPCQ

301 RYDQMLEALEKKVERIENNPRRRAKESKVREYEEKQFPEIRKQRELQERMQSRVQGRSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMY
301 RYDQMLEAWEKKVERIENNPRRRAKESKVREYEEKQFPEIRKQRELQERMQSRVQGRSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMY

401 DADQQRIFKFINMGLMADPMKVYKDRQVMNMWSEQEKETPREKFMQHPKFNGLIASFLERKTVAECVLYYYLTKKNYKSLVRRSYRRRGKSQQOQQQQ
401 DADQQRIFKFINMGLMDDPMKVYKDRQVTNMWSEQERDTPREKFMQHPKFNGLIASFLERKTVAECVLYYYLTKKNYKSLVRRSYRRRGKSQQOQQQQ

501 QQQQQQQQQPMPRSSQEEKDEKEKEKEAEKEEEKPEVENDKEDLLKEKTDGSDGNDKEA VASKGRKTANSQGRRKGRITRSMANEANSEEAITPQQ
501 QQQQQQQ ---MARSSQEEKEKEKEADKEEEKQDAENEKEELSKEKTDGSDGNDKEA VASKGRKTANSQGRRKGRITRSMANEANHEETATPQQ

601 SAELASMELESSRTEEMETAKKGLLEHGRNWSAIARMVSGKTSVQCKNFYFNKQRNLDLQHQHKLKMEKERNARRKKKAPAAASEEAFPPV
597 SSELASMEMESSRTEEMETAKKGLLEHGRNWSAIARMVSGKTSVQCKNFYFNKQRNLDLQHQHKLKMEKERNARRKKKTPAAASEETAFFPAA

701 EDEEMEASGVSGNEEMVEEAELHASGNEVPR - GECSGPATVNNSSDTEISPSHTEAAKDTGONGPKPPATLGADGPPGPPTPPRRTSRAPIEPTA
697 EDEEMEASGASANEELAEAEASQASGNEVPRVGECSGPAVNNSSDTEISVSPSRSEAMKDTG ---PKPTGTEALPAATQPPVPPPEPAVAPAEPSV

800 SEATGAPTPPPAPPSPSAPPVVPKEEKEETAAPP ---VEEGEEQKPPAAEE - LAVDTGKAEEP ---VKSECTEEAEEGA - KGKDAEAAEATAEGALK
794 PDASGPPSPPEPSSHLP - PRLWTRMNNKPRLLQLPRQMPRSRSLRPRRSMWEKPEEPEASEEPPESVKSDHKEETEEEPEDKAKGTEAETVSEAPLK

893 AEKKEGSGRATTAKSSGAPQSDSSATCSADEVDEAGDGKRLLSRPSLLTPTGDPANASPOKPLDLKQLKQRAAIPPIQVTKVHEPPREDAPT
893 VEE - AGSKAAVTGSSSGATQSDSFATCSADEVDEPEGDGKRLLSRPSLLTPTAGDPRASTSPQKPLDLKQLKQRAAIPPIQVTKVHEPPREDTVP

993 KPAPPAPPPQNLQPEDAPQPGSSPRGKSRSPAPPADKEA -----FAAEAKLPDPPCWTSGLPFPVPPPREVIKASPHAPDPSAFSYAPPGHPL
992 KPVPVPPPTQLQPEGDVSSQSGSPRGKSRSPVPAEKEAEKPAFFPAFTSGPKLPTEPPRWSSGLFPPIPPREVIKTSPHAADPSAFSYTPPGHPL

1095 PLGLHDTARVLP RPPTISNPPPLISSAKHPSVLERQIGAISSQ - GMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPPSGVKQEQLSPRGQAGPPES
1092 PLGLHDSARPVLP RPPTISNPPPLISSAKHPSVLERQIGAISSQ - GMSVQLRVPHSEHAKAPMGPLTMGLPLAVDPKKL -----

1184 LGVPTAQEASVLRGTALGSVPGGSITKGPSTRVPSDSAITYRGSITHGTADVLKYGTITRIIGEDSPSRDLRGREDSLPKGHVIEGKKGHVLSYEGG
1169 -----GTALGSATSGSITKGLPSTRAADGPS ---YRGSITHGTADVLKYGTISIRIVGEDSPSRDLRAREDTLPKGHVIEGKKGHVLSYEGG

1284 MSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHLKEQHHRGHSITQGI PRSYVEAQEDYLREAKLLKREGT h - SMRT
1254 MSVSQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRVTVSASIEGLMGRAIP - EQHSPH - LKEQHHRGHSITQGI PRSYVEAQEDYLREAKLLKREGT m - SMRT

1384 PPPPPSRDLTEAYKT ---QALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTGSKKHVDVRSIGSP h - SMRT
1352 PPPPPSRDLTEYKPRPLDPLGPKLKPTHEGVVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDSGAPSTGKKHVDVRSIGSP m - SMRT

1481 GRTFPVPHPLDVMADARALERACYEESLKSRTGASSSGSIARGAPVIVPELKGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKAS h - SMRT
1452 GRFPFALHPLDIMADARALERACYEESLKSRTGASSSGSITRGAPVVVPELKGKPRQSPLTYEDHGAPFTSHLPRGSPVTMREPTPRLQEGSLSSSKAS m - SMRT

1581 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVSGVDLYRSHIPLADPTSIPRGIPLDAAA - YYLPRHLAPNPTYPHLYPPYLIRGYPDTAAL h - SMRT
1552 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVSGVDLYRSHIPLADPTSIPRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGYPDTAAL m - SMRT

1690 ENRQTIINDYITSQMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPPTGTPATAMDRLAYLPTAPPPFSRHSSSPLSP h - SMRT
1652 ENRQTIINDYITSQMHNTAASAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPPTGTPATAIDRLAYLPTAPPPFSRHSSSPLSP m - SMRT

1780 GGPHTLTKPTTTSSSERERDRDRERDREREKSIILSTTTVEHAPIWRPGTEQSSGSSGSSGSSGSSRPAHSHAHQHSPI SPRTQDALQORPSVLH h - SMRT
1752 GGPHTLAKPTATSSSERERERERERD ---KSILSTTTVEHAPIWRPGTEQSSGAGGSS ---RPASHTQH ---SPISPTQDALQORPSVLH m - SMRT

1680 NTGMKGIIITAVEPSKPTVLR ---STSTSPVRPAATFPFATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS h - SMRT
1836 NTSKMGVTVSVEPGTPTVLRWARSTSTSSPVRPAATFPFATHCPLGGTLEGVYPTLMEPVLLPKETSRVARPERARVDAGHAFLTKPPGR ---EPASSPS m - SMRT

1977 KGSEPRPLVPPVSGHATIARTPAKNLAPHASPDPPAPPASADPHREKTQSKPFSIQELELRLSGYH - GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE h - SMRT
1933 KSSEPRSLAPPSSSHTAIARTPAKNLAPHASPDPPAPT - SASDLHREKTQSKPFSIQELELRLSGYHSGAGYSPDGVEFISPVSSPSLTHDKGLSKPLE m - SMRT

2076 ELDKSHLEGELRPKQPGPVKLGGAAHLPHLRPLPESQPSSSPLLQTPAGVKGHQVRVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLD h - SMRT
2032 ELEKSHLEGELRHKQPGPMKLSAAEAHLPHLRPLPESQPSSSPLLQTPAGIKGHQVRVTLAQHISEVITQDYTRHHPQQLSGPLPAPLYSFPGASCPVLD m - SMRT

2176 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEFVSPPEGMTEPGHRSRASYPLLYRDGEQTEPSRMGKSPGNTSQPPAFFSKL h - SMRT
2132 LRRPPSDLYLPPPDHGTPARGSPHSEGGKRSPEPKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQCEPR - MGLESNGNTSQPPTFFSKL m - SMRT

2276 TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGTGLMITYRSQAVQEHASTNMGLEAIIIRKALMGKYDQWEESPPLSANAFNPLNASE h - SMRT
2231 TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGAGLMTCSRQAVQEHASTNMGLEAIIIRKALMGKYDQWEESPPLGANAFNPLNASE m - SMRT

2376 SLPAA - MPITAADGRSDHTLTPGGGGKAKVSGRPSRRKAKSPAGLASGDRPPSVSSVHSEGDENRRTPLTNRVWEDRPSSAGSTFPFYNPLIMRLQAG h - SMRT
2331 SLPAAAMPITADGRSDHALTPGGGGKAKVSGRPSRRKAKSPAGLASGDRPPSVSSVHSEGDENRRTPLTNRVWEDRPSSAGSTFPFYNPLIMRLQAG m - SMRT

2475 VMASPPPPGLPAGSGPLAGPHHAWDEEPKPLLCQYETLSDSE h - SMRT
2431 VMASPPPPGLAAGSGPLAGPHHAWDEEPKPLLCQYETLSDSE m - SMRT

FIGURE 4

FIGURE 5A

FIGURE 5A

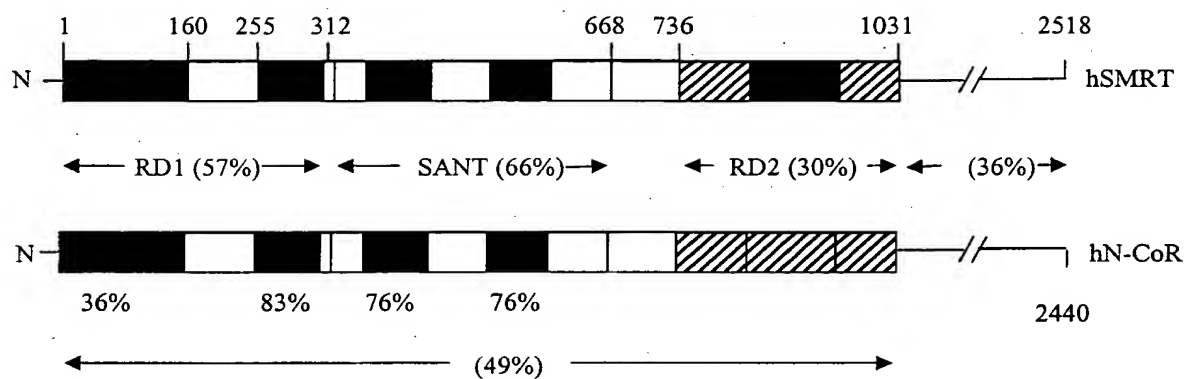


FIGURE 5B



FIGURE 6A

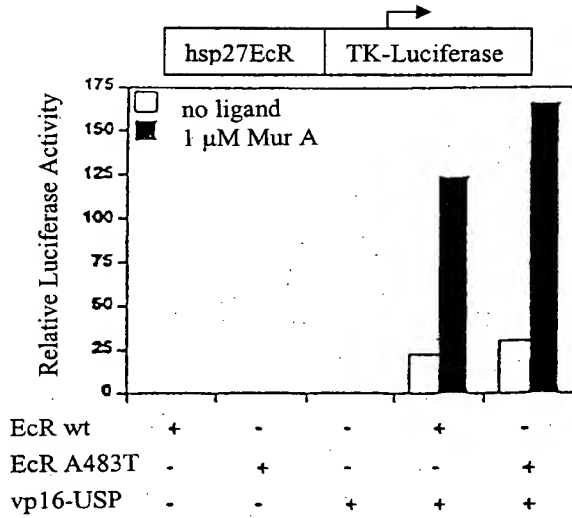


FIGURE 6B

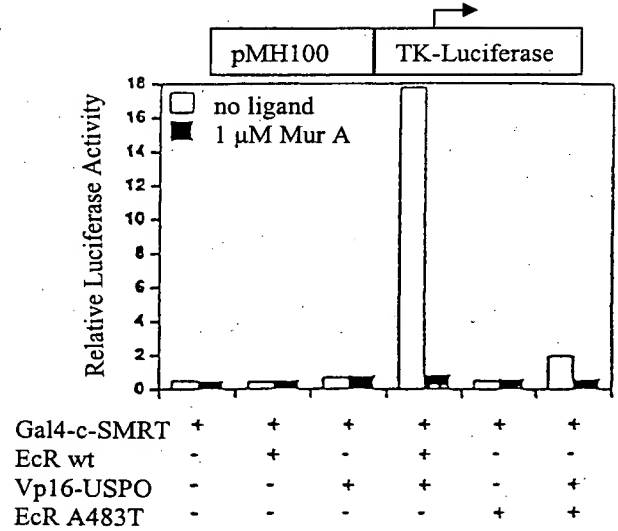
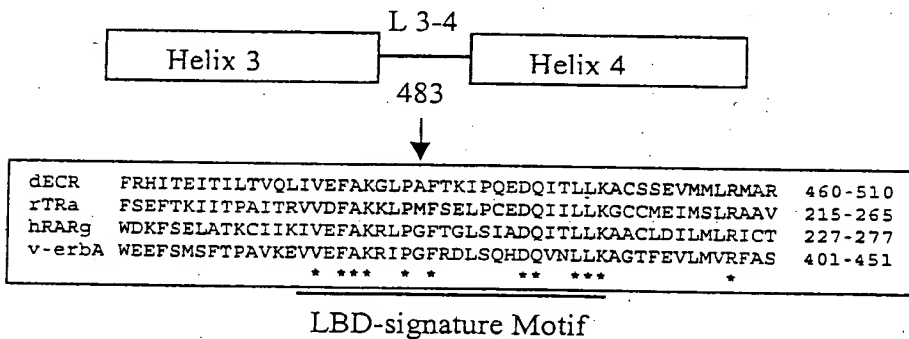


FIGURE 6C



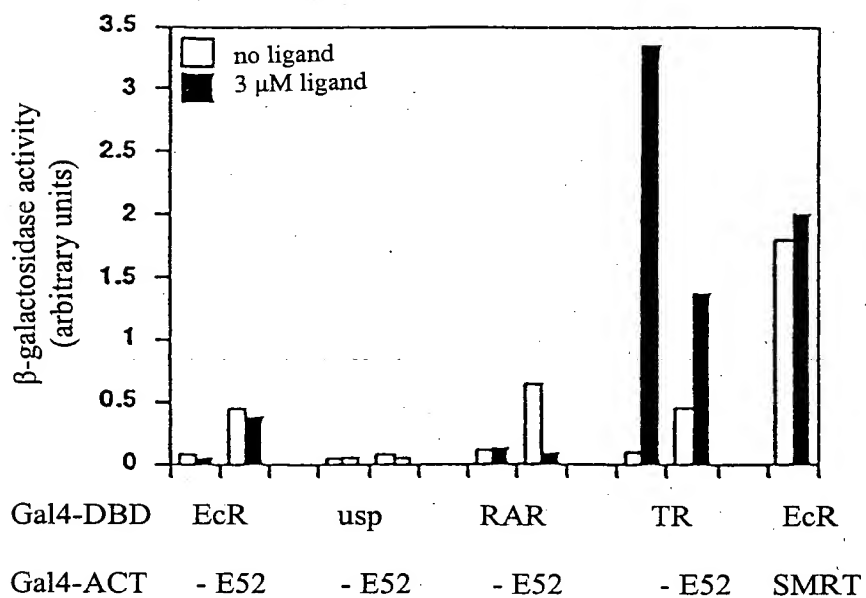


FIGURE 7

[illegible]



SNOR motif

SMRTER:	573	KEELLMQIQKVDNEIKSAETTMTLKKKEKSLMEEAALAKEQRAAKELND
mN-CoR:	177	KEELIQSMDRVVDREIAKVEQQIILKLLKKKQQQLEEEA--AKPPEPEKPVSP
hSMRT:	169	KEELIQNMDRVVDREITMVEQQISKLKKKQQQLEEEA--AKPPEPEKPVSP
SMRTER:	623	NNNDQEPMVLSWRSQMLAEKTYAANRRKTAQAQHSMLQNAADESSPGSV
mN-CoR:	226	-----PPVEQKHRS--IVQIIYDENRKKAEIAHKIFEGLGPKVE-----
hSMRT:	217	-----PPTESKHRS--LVQIIYDENRKKAEAAHRILEGGLGPOVE-----
SMRTER:	673	AGRPWLPLYNQHLVDVEALAMLIHQHOSQIRAPILLHIRKLLKAERWAHNNQG
mN-CoR:	263	-----LPLYNQPSDTRVYHENIKINQV-MRKKLILFKRRNHARKQREKQK
hSMRT:	254	-----LPLYNQPSDTRVYHENIKINQA-MRKKLILFKRRNHARKQWKQK
SMRTER:	723	LVEKYTKDQADWQRRICERMEASAKRKAREAKNREFFTEKVFTELKQREOK
mN-CoR:	307	ICORYDQLMFAWEKKVDRIENNPRRKAKESKTREYYEKQFPETRKQREQQ
hSMRT:	298	FCORYDQLMFALEKKVERIENNPRRKAKESKVREYYEKQFPETRKQRELO
SMRTER:	773	ERFN-RVGSR-----IKSEADLEEIMDGLQEQALEDKMRSYAVIPP
mN-CoR:	357	ERFQ-RVGQRGAGLSATIRSEHEISEIIDGLSEQENNEKQMRQLSVIPP
hSMRT:	348	ERMOSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPP
SMRTER:	814	LMHDARQRRCAVHNENGLIEDMVAVHQQRKALNM
mN-CoR:	406	MMFDARQRRVVKFINMNGLMEDPMKVYKDRQFMNV
hSMRT:	398	MLYDADQORIKFINMNGLMADPMKVYKDRQVMNM

SANT domain

SMRTER	:848	WTAGEKETFKKYLQHPKNFNGATAASLDR-KSPQDCVRYFYLSKKKTENY	100%
mN-CoR(1)	:440	WTDHEKEIFKDKFIQHPKNFGLIASYLER-KSVPCVLYFYLTKKKNENY	68/80%
hSMRT(1)	:432	WSEQEKETFREKFMQHPKNFGLIASFLER-KTVAECVLYFYLTKKKNENY	64/82%
C14B9.6	:615	WSPEERSLFLKSRQADHVKIFHGLTEFFVD-KTASDLVLFYFMNKKTEDY	35/53%
Cf53H10	:218	WTPDEIYQFQDAIYQSEKDFDKVAVELPG-KSVMECVQFYTWKKDCPD	38/56%
xER1	:277	WTEEECRNFEQGLKAIGKDFHLITQANKVTRTSVGECAVAFYMWKKSERV	36/56%
mN-CoR(2)	:627	WTEEEEMEVAKKGLVEHGRNWAATAK-MVGTKSEADCKNFYFNKRRHNL	34/53%
hSMRT(2)	:615	WTEEEEMETAKKGLLEHGRNWSATAK-MVGSKTYSQCKNFYFNKRRNL	38/57%
hKIAA0071	:106	WTVKQKVLFEQAFSPHISKIFHRIQOMLPD-KSIASLVKFFYSWKKIRTK	37/50%
CMTA-I	:198	WTDQEIITLFENCYQIFGKNFSQIRSEALCH-RSLOSIVQFYYESKKRVKY	39/51%
YCR592	:673	ETDHEHSLFLLEGYLITHEKFFGKISHVMGGLRSPEDCVLHYRTKKTVNY	46/62%

α-helix

α-helix

ITS motif

SMRTER:	2424	TRQIVMHDYITSQQMQ
SMRT:	1681	NROTIINDYITSQQMH
N-CoR:	1615	TRQTIINDYITSQQMQ

GSI motif

SMRTER:	2274	VKSGSIIHGTPANS
	2236	GKHGSITQGTPLHM
SMRT:	1203	VPGGSITKGTIPSTR
	1224	TYRGSITHGTPADV
	1350	HIRGSITQGTIPRSY
	1446	LKEGSITQGTPLKY
	1517	SSGGSIIARGAPVIV
N-CoR:	921	TPPGSILISSPIKP
	1064	IMGGSISQGTPTGT
	1092	PSVGSISLGLPRQO
	1149	VQEGSITRGTPASK
	1171	SLRGSITQGTPLP
	1302	VLSGSIMOGTPRAT
	1388	IIEGSISQGTPIKF
C14B9.6:	920	QTQGSLSGTPTFQA

LSD motif

SMRTER:	3430	ESKPLLLSKYDALSD-ED
SMRT:	2501	EPKPLLCQYETLSDSE
N-CoR:	2436	EPAPLLSAQYETLSDSD

FIGURE 9

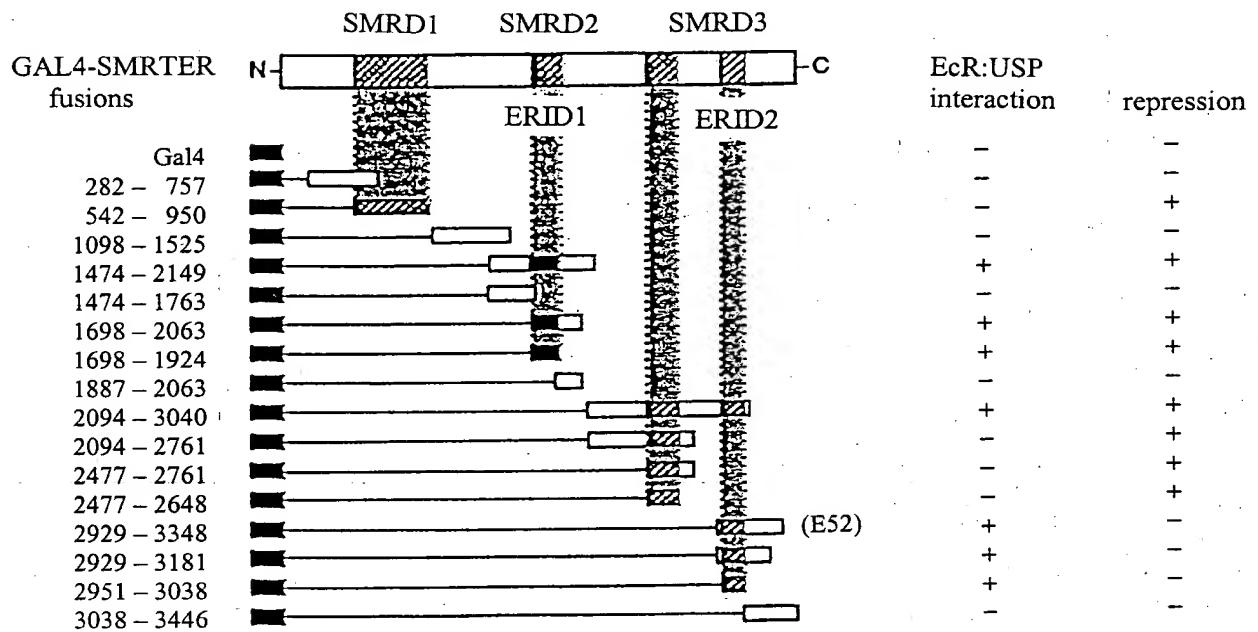


FIGURE 10



FIGURE 11A

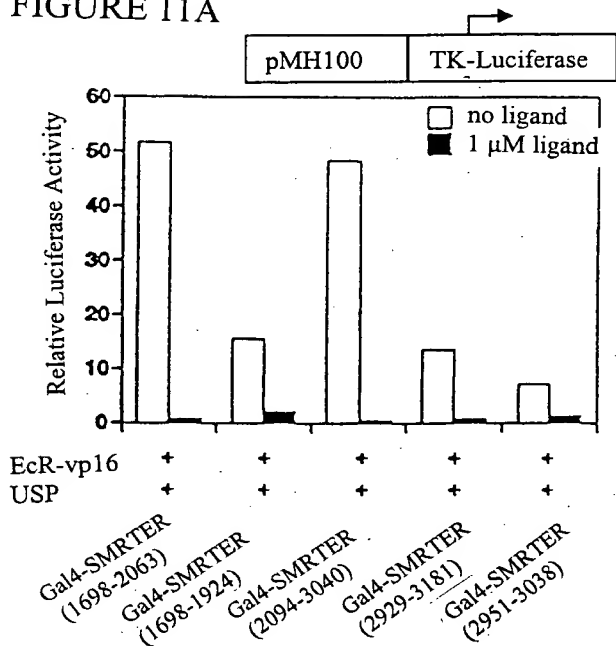


FIGURE 11B

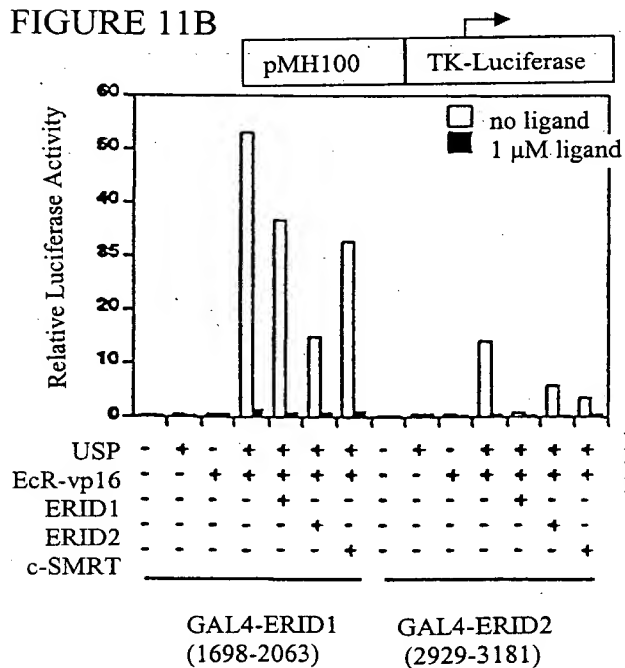


FIGURE 11C

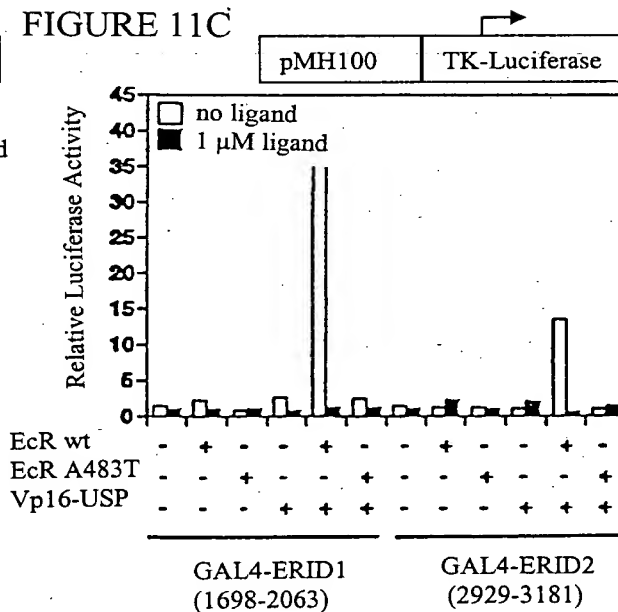


FIGURE 12A

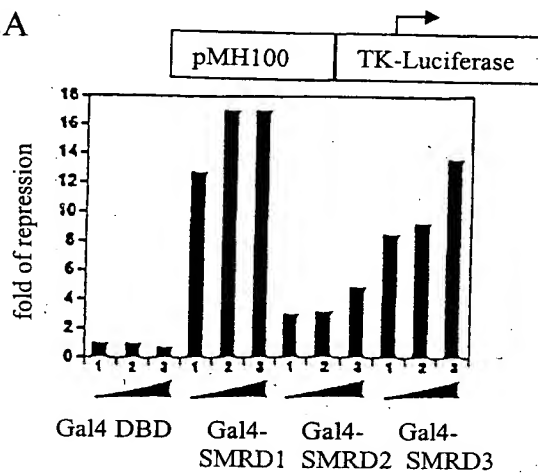


FIGURE 12B

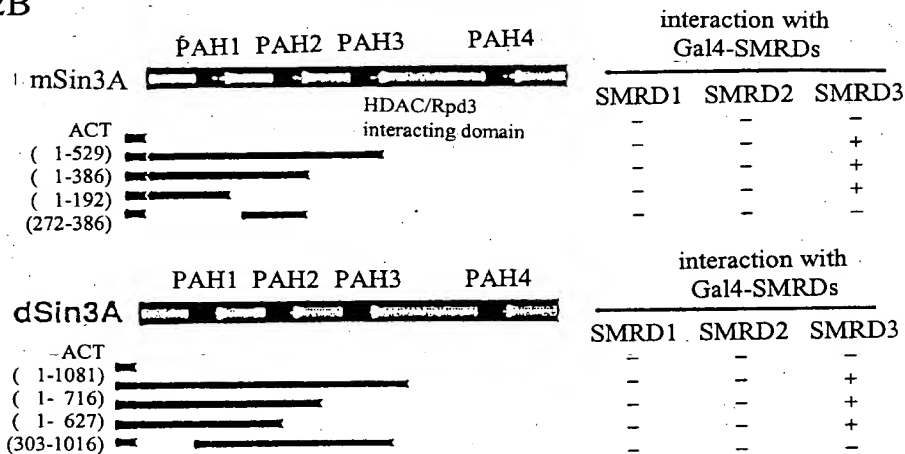


FIGURE 12C

